



SEQUENCE LISTING

<110> THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
KORNBLUTH, Richard S.

<120> MULTIMERIC FUSION PROTEINS OF TNF SUPERFAMILY LIGANDS (AMENDED)

<130> UCSD1590

<140> US 09/454,223
<141> 1999-12-09

<150> US 60/111,471
<151> 1998-12-09

<160> 22

<170> PatentIn version 3.1

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<223> Murine surfactant protein D (without the CRD) fused to the
extracellular portion of human CD40L

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<221> 5'UTR
<222> (7)..(31)

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<221> sig_peptide
<222> (32)..(88)
<223> Signal peptide from murine surfactant protein D

<220>
<221> misc_feature
<222> (88)..(799)
<223> Mature murine surfactant protein D including hub region,
collagenous portion, and neck, but excluding carbohydrate
recognition domain (CRD)

<220>
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<222> (801)..(1546)
<223> Human CD40 ligand extracellular region, including stalk.

<300>
<301> Motwani M
<302> Mouse surfactant protein-D. cDNA cloning, characterization, and
gene localization to chromosome 14.
<303> J. Immunol.
<304> 155
<305> 12

<306> 5671 TO 5677
 <307> 1995
 <313> (32)..(802)

<300>
 <301> Spriggs MK
 <302> Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobulin E secretion
 <303> Journal of Experimental Medicine
 <304> 176
 <305> 6
 <306> 1543-1550
 <307> 1992
 <313> (803)..(1552)

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agc ctc tcg cag aga tca gta ccc aac acc tgc acc cta gtc atg tgt 148
 Ser Leu Ser Gln Arg Ser Val Pro Asn Thr Cys Thr Leu Val Met Cys
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 Ser Pro Thr Glu Asn Gly Leu Pro Gly Arg Asp Gly Arg Asp Gly Arg
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gaa ggt cca cgg ggt gag aag ggt gat cca ggt ttg cca gga cct atg 244
 Glu Gly Pro Arg Gly Glu Lys Gly Asp Pro Gly Leu Pro Gly Pro Met
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gag aat ggc tct gct ggc gaa cct gga cca aag gga gaa cgt gga cta 340
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agt gga cct cca gga ctt cca ggt att cct ggt cca gct ggg aaa gaa 388
 Ser Gly Pro Pro Gly Leu Pro Gly Ile Pro Gly Pro Ala Gly Lys Glu
 105 110 115

ggt ccc tct ggg aag cag ggg aac ata gga cct caa ggc aaa cca ggt 436
 Gly Pro Ser Gly Lys Gln Gly Asn Ile Gly Pro Gln Gly Lys Pro Gly
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cct aaa gga gag gct ggg ccc aaa gga gaa gta ggt gct cct ggc atg 484
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Pro	Gly	Leu	Lys	Gly	Asp	Arg	Gly	Val	Pro	Gly	Asp	Arg	Gly	Ile	Lys		
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Pro Gly Leu Pro Gly Pro Met Gly Leu Ser Gly Leu Gln Gly Pro Thr
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Pro Lys Gly Glu Arg Gly Leu Ser Gly Pro Pro Gly Leu Pro Gly Ile
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Pro Gly Pro Ala Gly Lys Glu Gly Pro Ser Gly Lys Gln Gly Asn Ile
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Glu Val Gly Ala Pro Gly Met Gln Gly Ser Thr Gly Ala Lys Gly Ser
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Thr Gly Pro Lys Gly Glu Arg Gly Ala Pro Gly Val Gln Gly Ala Pro
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Gly Asn Ala Gly Ala Ala Gly Pro Ala Gly Pro Ala Gly Pro Gln Gly
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Ala Pro Gly Ser Arg Gly Pro Pro Gly Leu Lys Gly Asp Arg Gly Val
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Pro Gly Asp Arg Gly Ile Lys Gly Glu Ser Gly Leu Pro Asp Ser Ala
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Ala Leu Arg Gln Gln Met Glu Ala Leu Lys Gly Lys Leu Gln Arg Leu
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Glu Val Ala Phe Ser His Tyr Gln Lys Ala Ala Leu Phe Pro Asp Gly
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His Arg Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp
 260 265 270

Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser
 275 280 285

Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe
 290 295 300

Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser
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Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val
 325 330 335

Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu
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Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln

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<223> Murine surfactant protein D including hub region, collagenous
portion, and neck, but excluding carbohydrate recognition domain
(CRD)

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<300>
<301> Anderson, DM
<302> A homologue of the TNF receptor and its ligand enhance T-cell
growth and dendritic-cell function.
<303> Nature
<304> 390
<305> 6656
<306> 175-179
<307> 1997
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cca gga ctc aag ggg gac aga ggt gtt cct gga gac aga gga atc aaa Pro Gly Leu Lys Gly Asp Arg Gly Val Pro Gly Asp Arg Gly Ile Lys			676
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cag aaa gct gca ttg ttc cct gat gga cga gcg cag atg gat cct aac Gln Lys Ala Ala Leu Phe Pro Asp Gly Arg Ala Gln Met Asp Pro Asn			820
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cat gaa aac gca ggt ttg cag gac tcg act ctg gag agt gaa gac aca His Glu Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr			916
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Thr Cys Thr Leu Val Met Cys Ser Pro Thr Glu Asn Gly Leu Pro Gly
 35 40 45

Arg Asp Gly Arg Asp Gly Arg Glu Gly Pro Arg Gly Glu Lys Gly Asp
 50 55 60

Pro Gly Leu Pro Gly Pro Met Gly Leu Ser Gly Leu Gln Gly Pro Thr
 65 70 75 80

Gly Pro Val Gly Pro Lys Gly Glu Asn Gly Ser Ala Gly Glu Pro Gly
85 90 95

Pro Lys Gly Glu Arg Gly Leu Ser Gly Pro Pro Gly Leu Pro Gly Ile
100 105 110

Pro Gly Pro Ala Gly Lys Glu Gly Pro Ser Gly Lys Gln Gly Asn Ile
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Gly Pro Gln Gly Lys Pro Gly Pro Lys Gly Glu Ala Gly Pro Lys Gly
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Glu Val Gly Ala Pro Gly Met Gln Gly Ser Thr Gly Ala Lys Gly Ser
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Thr Gly Pro Lys Gly Glu Arg Gly Ala Pro Gly Val Gln Gly Ala Pro
165 170 175

Gly Asn Ala Gly Ala Ala Gly Pro Ala Gly Pro Ala Gly Pro Gln Gly
180 185 190

Ala Pro Gly Ser Arg Gly Pro Pro Gly Leu Lys Gly Asp Arg Gly Val
195 200 205

Pro Gly Asp Arg Gly Ile Lys Gly Glu Ser Gly Leu Pro Asp Ser Ala
210 215 220

Ala Leu Arg Gln Gln Met Glu Ala Leu Lys Gly Lys Leu Gln Arg Leu
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Glu Val Ala Phe Ser His Tyr Gln Lys Ala Ala Leu Phe Pro Asp Gly
245 250 255

Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His Cys
260 265 270

Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Gly Leu Gln Asp Ser
275 280 285

Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met Lys
290 295 300

Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly
305 310 315 320

Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp Leu
 325 330 335

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 355 360 365

Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr
 370 375 380

Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr Leu
 385 390 395 400

Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val Pro
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Val Gln Asp Ile Asp
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<301> Motwani M
<302> Mouse surfactant protein-D. cDNA clonings, characterization, and
gene localization to chromosome 14.
<303> Nature
<304> 357
<305> 6373
<306> 80 TO 82
<307> 1992-05-07
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<300>
<301> Armitage RJ
<302> Molecular and biological characterization of a murine ligand for
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<303> Nature
<304> 357
<305> 6373
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Ser Leu Ser Gln Arg Ser Val Pro Asn Thr Cys Thr Leu Val Met Cys
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agc cca aca gag aat ggc ctg cct ggt cgt gat gga cgg gat ggg aga      196
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Glu Gly Pro Arg Gly Glu Lys Gly Asp Pro Gly Leu Pro Gly Pro Met
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Ser Gly Pro Pro Gly Leu Pro Gly Ile Pro Gly Pro Ala Gly Lys Glu	
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235 240 245	
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Gln Lys Ala Ala Leu Phe Pro Asp Gly His Arg Arg Leu Asp Lys Val	
250 255 260	
gaa gag gaa gta aac ctt cat gaa gat ttt gta ttc ata aaa aag cta	868
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Lys Arg Cys Asn Lys Gly Glu Gly Ser Leu Ser Leu Leu Asn Cys Glu	
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gag atg aga agg caa ttt gaa gac ctt gtc aag gat ata acg tta aac	964
Glu Met Arg Arg Gln Phe Glu Asp Leu Val Lys Asp Ile Thr Leu Asn	
300 305 310	

```

aaa gaa gag aaa aaa gaa aac agc ttt gaa atg caa aga ggt gat gag      1012
Lys Glu Glu Lys Lys Glu Asn Ser Phe Glu Met Gln Arg Gly Asp Glu
          315                      320                      325

gat cct caa att gca gca cac gtt gta agc gaa gcc aac agt aat gca      1060
Asp Pro Gln Ile Ala Ala His Val Val Ser Glu Ala Asn Ser Asn Ala
          330                      335                      340

gca tcc gtt cta cag tgg gcc aag aaa gga tat tat acc atg aaa agc      1108
Ala Ser Val Leu Gln Trp Ala Lys Lys Gly Tyr Tyr Thr Met Lys Ser
          345                      350                      355

aac ttg gta atg ctt gaa aat ggg aaa cag ctg acg gtt aaa aga gaa      1156
Asn Leu Val Met Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Glu
          360                      365                      370                      375

gga ctc tat tat gtc tac act caa gtc acc ttc tgc tct aat cgg gag      1204
Gly Leu Tyr Tyr Val Tyr Thr Gln Val Thr Phe Cys Ser Asn Arg Glu
          380                      385                      390

cct tcg agt caa cgc cca ttc atc gtc ggc ctc tgg ctg aag ccc agc      1252
Pro Ser Ser Gln Arg Pro Phe Ile Val Gly Leu Trp Leu Lys Pro Ser
          395                      400                      405

att gga tct gag aga atc tta ctc aag gcg gca aat acc cac agt tcc      1300
Ile Gly Ser Glu Arg Ile Leu Leu Lys Ala Ala Asn Thr His Ser Ser
          410                      415                      420

tcc cag ctt tgc gag cag cag tct gtt cac ttg ggc gga gtg ttt gaa      1348
Ser Gln Leu Cys Glu Gln Gln Ser Val His Leu Gly Gly Val Phe Glu
          425                      430                      435

tta caa gct ggt gct tct gtg ttt gtc aac gtg act gaa gca agc caa      1396
Leu Gln Ala Gly Ala Ser Val Phe Val Asn Val Thr Glu Ala Ser Gln
          440                      445                      450                      455

gtg atc cac aga gtt ggc ttc tca tct ttt ggc tta ctc aaa ctc      1441
Val Ile His Arg Val Gly Phe Ser Ser Phe Gly Leu Leu Lys Leu
          460                      465                      470

tgaacagtgc gctgtcctag gctgcagcag ggtacc      1477

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<210> 6
<211> 470
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic Construct

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<400> 6

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Met Leu Pro Phe Leu Ser Met Leu Val Leu Leu Val Gln Pro Leu Gly
1          5          10          15

```

```

Asn Leu Gly Ala Glu Met Lys Ser Leu Ser Gln Arg Ser Val Pro Asn
          20          25          30

```

Thr Cys Thr Leu Val Met Cys Ser Pro Thr Glu Asn Gly Leu Pro Gly
 35 40 45

Arg Asp Gly Arg Asp Gly Arg Glu Gly Pro Arg Gly Glu Lys Gly Asp
 50 55 60

Pro Gly Leu Pro Gly Pro Met Gly Leu Ser Gly Leu Gln Gly Pro Thr
 65 70 75 80

Gly Pro Val Gly Pro Lys Gly Glu Asn Gly Ser Ala Gly Glu Pro Gly
 85 90 95

Pro Lys Gly Glu Arg Gly Leu Ser Gly Pro Pro Gly Leu Pro Gly Ile
 100 105 110

Pro Gly Pro Ala Gly Lys Glu Gly Pro Ser Gly Lys Gln Gly Asn Ile
 115 120 125

Gly Pro Gln Gly Lys Pro Gly Pro Lys Gly Glu Ala Gly Pro Lys Gly
 130 135 140

Glu Val Gly Ala Pro Gly Met Gln Gly Ser Thr Gly Ala Lys Gly Ser
 145 150 155 160

Thr Gly Pro Lys Gly Glu Arg Gly Ala Pro Gly Val Gln Gly Ala Pro
 165 170 175

Gly Asn Ala Gly Ala Ala Gly Pro Ala Gly Pro Ala Gly Pro Gln Gly
 180 185 190

Ala Pro Gly Ser Arg Gly Pro Pro Gly Leu Lys Gly Asp Arg Gly Val
 195 200 205

Pro Gly Asp Arg Gly Ile Lys Gly Glu Ser Gly Leu Pro Asp Ser Ala
 210 215 220

Ala Leu Arg Gln Gln Met Glu Ala Leu Lys Gly Lys Leu Gln Arg Leu
 225 230 235 240

Glu Val Ala Phe Ser His Tyr Gln Lys Ala Ala Leu Phe Pro Asp Gly
 245 250 255

His Arg Arg Leu Asp Lys Val Glu Glu Glu Val Asn Leu His Glu Asp
 260 265 270

Phe Val Phe Ile Lys Lys Leu Lys Arg Cys Asn Lys Gly Glu Gly Ser

```

275                280                285

Leu Ser Leu Leu Asn Cys Glu Glu Met Arg Arg Gln Phe Glu Asp Leu
290                295                300

Val Lys Asp Ile Thr Leu Asn Lys Glu Glu Lys Lys Glu Asn Ser Phe
305                310                315                320

Glu Met Gln Arg Gly Asp Glu Asp Pro Gln Ile Ala Ala His Val Val
325                330                335

Ser Glu Ala Asn Ser Asn Ala Ala Ser Val Leu Gln Trp Ala Lys Lys
340                345                350

Gly Tyr Tyr Thr Met Lys Ser Asn Leu Val Met Leu Glu Asn Gly Lys
355                360                365

Gln Leu Thr Val Lys Arg Glu Gly Leu Tyr Tyr Val Tyr Thr Gln Val
370                375                380

Thr Phe Cys Ser Asn Arg Glu Pro Ser Ser Gln Arg Pro Phe Ile Val
385                390                395                400

Gly Leu Trp Leu Lys Pro Ser Ile Gly Ser Glu Arg Ile Leu Leu Lys
405                410                415

Ala Ala Asn Thr His Ser Ser Ser Gln Leu Cys Glu Gln Gln Ser Val
420                425                430

His Leu Gly Gly Val Phe Glu Leu Gln Ala Gly Ala Ser Val Phe Val
435                440                445

Asn Val Thr Glu Ala Ser Gln Val Ile His Arg Val Gly Phe Ser Ser
450                455                460

Phe Gly Leu Leu Lys Leu
465                470

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<210> 7
<211> 27
<212> DNA
<213> Artificial sequence

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<220>
<223> PCR primer

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<400> 7
ctgacatgct gccctttctc tccatgc

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<210> 8
 <211> 29
 <212> DNA
 <213> Artificial sequence

<220>
 <223> PCR primer

<400> 8
 ggaggccagc tgcctccag cctgtttgc 29

<210> 9
 <211> 56
 <212> DNA
 <213> Artificial sequence

<220>
 <223> PCR primer

<400> 9
 ggggctagcg aattccacca ggaagcaatc tgacatgctg ccctttctct ccatgc 56

<210> 10
 <211> 48
 <212> DNA
 <213> Artificial sequence

<220>
 <223> PCR primer

<400> 10
 tctatcttgt ccaaccttct atggccatca gggaacaatg cagctttc 48

<210> 11
 <211> 49
 <212> DNA
 <213> Artificial sequence

<220>
 <223> PCR primer

<400> 11
 aaagctgcat tgttccctga tggccataga aggttggaca agatagaag 49

<210> 12
 <211> 41
 <212> DNA
 <213> Artificial sequence

<220>
 <223> PCR primer

<400> 12
 gggctcgagg taccagttct acatgccttg gagtgtataa t 41

<210> 13
 <211> 50
 <212> DNA
 <213> Artificial sequence

<220>
 <223> PCR primer

<400> 13
 gaaagctgca ttgttccctg atggccatag aagattggat aaggtcgaag 50

<210> 14
 <211> 50
 <212> DNA
 <213> Artificial sequence

<220>
 <223> PCR primer

<400> 14
 cttcgacctt atccaatctt ctatggccat caggaacaa tgcagctttc 50

<210> 15
 <211> 34
 <212> DNA
 <213> Artificial sequence

<220>
 <223> PCR primer

<400> 15
 ggggggtacc ctgctgcagc ctaggacagc gcac 34

<210> 16
 <211> 16
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Fusion segment of SPD and CD40L sequence region

<400> 16

Lys	Ala	Ala	Leu	Phe	Pro	Asp	Gly	His	Arg	Arg	Leu	Asp	Lys	Ile	Glu
1				5					10					15	

<210> 17
 <211> 16
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Fusion segment of SPD and murine CD40L sequence region

<400> 17

Lys Ala Ala Leu Phe Pro Asp Gly His Arg Arg Leu Asp Lys Val Glu
 1 5 10 15

<210> 18
 <211> 19
 <212> DNA
 <213> Artificial sequence

<220>
 <223> PCR primer

<400> 18
 catgttctctg gccctcctc 19

<210> 19
 <211> 22
 <212> DNA
 <213> Artificial sequence

<220>
 <223> PCR primer

<400> 19
 gtacaggctc aagagagagg gc 22

<210> 20
 <211> 26
 <212> DNA
 <213> Artificial sequence

<220>
 <223> PCR primer

<400> 20
 atactcgagc gcagatggat cctaac 26

<210> 21
 <211> 38
 <212> DNA
 <213> Artificial sequence

<220>
 <223> PCR primer

<400> 21
 ggggttttagc ggccgctaata gttccacgaa atgagttc 38

<210> 22
 <211> 16
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Fusion sequence of SPD and RANKL/TRANCE sequence region

<400> 22

Lys Ala Ala Leu Phe Pro Asp Gly Arg Ala Gln Met Asp Pro Asn Arg
1 5 10 15